

7.0 SEQUENCE LISTING

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(1) GENERAL INFORMATION:

(i) APPLICANT: Baum, James A.
Gilmer, Amy Jelen
Mettus, Anne-Marie Light

(ii) TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
LEPIDOPTERAN-ACTIVE- δ -ENDOTOXINS

(iii) NUMBER OF SEQUENCES: 76

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee
(B) STREET: P.O. Box 4433
(C) CITY: Houston
(D) STATE: Texas
(E) COUNTRY: USA
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE:
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/757,536
(B) FILING DATE: 27-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kitchell, Barbara S.
(B) REGISTRATION NUMBER: 33,928
(C) REFERENCE/DOCKET NUMBER: MECO:206

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 512/418-3000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..3567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT	48
	Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	
	1 5 10 15	
15	AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT	96
	Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	
	20 25 30	
20	TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC	144
	Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	
	35 40 45	
25	TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG	192
	Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	
	50 55 60	
30	GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA	240
	Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	
	65 70 75 80	
35	CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT	288
	Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	
	85 90 95	
40	GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA	336
	Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	
	100 105 110	
45	TTT AAA GAA TGG GAA GAA GAT CCT AAT AAT CCA GCA ACC AGG ACC AGA	384
	Phe Lys Glu Trp Glu Glu Asp Pro Asn Asn Pro Ala Thr Arg Thr Arg	
	115 120 125	
50	GTA ATT GAT CGC TTT CGT ATA CTT GAT GGG CTA CTT GAA AGG GAC ATT	432
	Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile	
	130 135 140	
55	CCT TCG TTT GCA ATT TCT GGA TTT GAA GTA CCC CTT TTA TCC GTT TAT	480
	Pro Ser Phe Ala Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr	
	145 150 155 160	
60	GCT CAA GCG GCC AAT CTG CAT CTA GCT ATA TTA AGA GAT TCT GTA ATT	528
	Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile	
	165 170 175	

	TTT GGA GAA AGA TGG GGA TTG ACA ACG ATA AAT GTC AAT GAA AAC TAT	576
	Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr	
	180 185 190	
5	AAT AGA CTA ATT AGG CAT ATT GAT GAA TAT GCT GAT CAC TGT GCA AAT	624
	Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn	
	195 200 205	
10	ACG TAT AAT CGG GGA TTA AAT AAT TTA CCG AAA TCT ACG TAT CAA GAT	672
	Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp	
	210 215 220	
15	TGG ATA ACA TAT AAT CGA TTA CGG AGA GAC TTA ACA TTG ACT GTA TTA	720
	Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu	
	225 230 235 240	
20	GAT ATC GCC GCT TTC TTT CCA AAC TAT GAC AAT AGG AGA TAT CCA ATT	768
	Asp Ile Ala Ala Phe Phe Pro Asn Tyr Asp Asn Arg Arg Tyr Pro Ile	
	245 250 255	
25	CAG CCA GTT GGT CAA CTA ACA AGG GAA GTT TAT ACG GAC CCA TTA ATT	816
	Gln Pro Val Gly Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Ile	
	260 265 270	
30	AAT TTT AAT CCA CAG TTA CAG TCT GTA GCT CAA TTA CCT ACT TTT AAC	864
	Asn Phe Asn Pro Gln Leu Gln Ser Val Ala Gln Leu Pro Thr Phe Asn	
	275 280 285	
35	GTT ATG GAG AGC AGC GCA ATT AGA AAT CCT CAT TTA TTT GAT ATA TTG	912
	Val Met Glu Ser Ser Ala Ile Arg Asn Pro His Leu Phe Asp Ile Leu	
	290 295 300	
40	AAT AAT CTT ACA ATC TTT ACG GAT TGG TTT AGT GTT GGA CGC AAT TTT	960
	Asn Asn Leu Thr Ile Phe Thr Asp Trp Phe Ser Val Gly Arg Asn Phe	
	305 310 315 320	
45	TAT TGG GGA GGA CAT CGA GTA ATA TCT AGC CTT ATA GGA GGT GGT AAC	1008
	Tyr Trp Gly Gly His Arg Val Ile Ser Ser Leu Ile Gly Gly Gly Asn	
	325 330 335	
50	ATA ACA TCT CCT ATA TAT GGA AGA GAG GCG AAC CAG GAG CCT CCA AGA	1056
	Ile Thr Ser Pro Ile Tyr Gly Arg Glu Ala Asn Gln Glu Pro Pro Arg	
	340 345 350	
55	TCC TTT ACT TTT AAT GGA CCG GTA TTT AGG ACT TTA TCA AAT CCT ACT	1104
	Ser Phe Thr Phe Asn Gly Pro Val Phe Arg Thr Leu Ser Asn Pro Thr	
	355 360 365	
60	TTA CGA TTA TTA CAG CAA CCT TGG CCA GCG CCA CCA TTT AAT TTA CGT	1152
	Leu Arg Leu Leu Gln Gln Pro Trp Pro Ala Pro Pro Phe Asn Leu Arg	
	370 375 380	